



The *cis*-AB01 Allele Originated From the A105 Allele, and not From the A102 Allele

Sung-Jin Yang, M.D.^{1,*}, Eun Jeong Won, M.D.^{1,*}, Duck Cho, M.D.^{1,2}, Myung-Geun Shin, M.D.^{1,2}, and Dong-Wook Ryang, M.D.¹

Department of Laboratory Medicine¹, Chonnam National University Medical School, Gwangju; Department of Laboratory Medicine², Chonnam National University Hwasun Hospital, Hwasun, Korea

Researchers in the field of transfusion medicine have a growing interest in the *cis*-AB blood group, which is characterized by a paradoxical inheritance of the ABO blood group [1]. The *cis*-AB blood group arises from a glycosyltransferase capable of synthesizing both A and B antigens simultaneously [2]. In addition, affected individuals display more than one phenotype depending on their partnering alleles. *Cis*-AB may eventually lead to ABO discrepancy [3]. The *cis*-AB allele was the most common ABO subgroup in Korean blood donors [4], and Cho *et al.* [5] found that the *cis*-AB allele was also the most common cause of ABO discrepancy in Koreans. From similar contexts, many authors have performed genetic analysis of *cis*-AB with sequencing methods for ABO genotyping. These studies have suggested that the *cis*-AB01 allele arises from a single polymorphism, 803G>C, in exon 7 of the A102 allele [6, 7]. However, the sequencing was solely focused on exons 6 and 7. According to a previous study, analysis of intron sequences indicated that individuals with the A102 allele may be re-classified into those with the A105 allele [8]. We therefore performed an extended analysis of the genomic sequences of the *cis*-AB01 allele, previously known as the A102 allele, to clarify its genetic background.

Here, we screened five samples of the *cis*-AB01 allele through

direct sequencing of exons 6 and 7 from samples submitted for ABO genotyping between January 2009 and December 2011 to Chonnam National University Hospital and Chonnam National University Hwasun Hospital. We performed ABO genotyping for all exons and introns except intron 1 and then compared the *cis*-AB01 and A101 allele sequences. This analysis showed identical point mutations in the *cis*-AB01, compared to A101 alleles (1142C>T in intron 4, 163T>C and 179C>T in intron 6, 467C>T and 803G>C in exon 7). We found only one nucleotide difference between the *cis*-AB01 allele and the A105 allele, 803G>C, in contrast to the three nucleotides that differed between the *cis*-AB01 and A102 alleles. Based on the prevailing hypothesis that mutations in the ABO gene render it capable of synthesizing both A and B antigens, our data led to the speculation that the A105 allele might have acquired a single point mutation at 803G>C in exon 7 and got converted to the *cis*-AB01 allele (Fig. 1). We found that the frequencies of the A101, A102, A105, O01, and O02 alleles were 3.3%, 33.3%, 23.3%, 20.0%, and 20.0%, respectively, in specimens (n=15) collected from individuals with the normal A phenotype. Thus, although A105 allele is the second most prevalent among A alleles, we assume that, without analysis of intron 6 sequences, the A105 allele can be mistaken

Received: September 5, 2014
Revision received: October 15, 2014
Accepted: December 29, 2014

Corresponding author: Dong-Wook Ryang
Department of Laboratory Medicine, Chonnam National University Medical School, 42 Jebong-ro, Dong-gu, Gwangju 501-757, Korea
Tel: +82-62-220-5340, Fax: +82-62-224-2518
E-mail: dwryang@chonnam.ac.kr

*Yang SJ and Won EJ contributed equally to this work.

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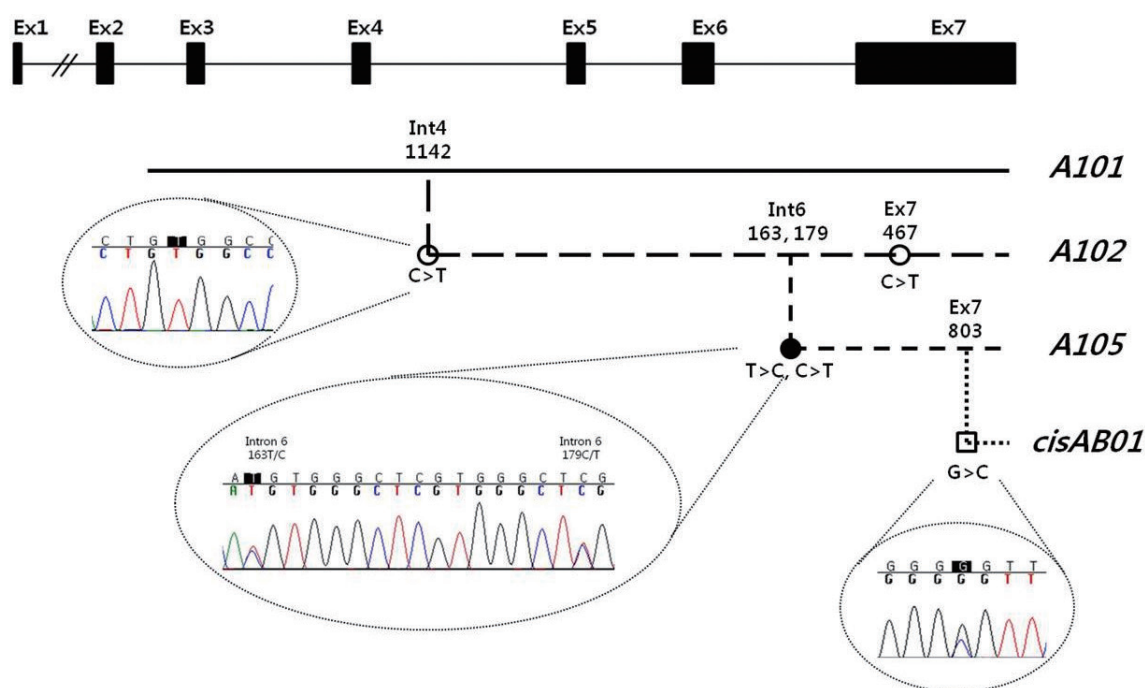


Fig. 1. The molecular origin of the *cis-ABO1* allele is the *A105* allele, but not the *A102* allele. The *cis-ABO1* allele has five point mutations compared to the *A101* allele as follows: 1142C>T in intron 4, 163T>C and 179C>T in intron 6, 467C>T and 803G>C in exon 7. The *cis-ABO1* allele has the only one nucleotide difference of 803G>C compared with the *A105* allele.

Abbreviations: Ex, exon; Int, intron.

for the *A102* allele. Genetic analysis of exons 6 and 7 has been commonly used for demonstrating a new allele [6, 7, 9]; however, our results indicate that further studies are warranted to analyze lineage-specific variations in intron sequences, intron 6 in particular, which is essential for obtaining accurate results of the ABO genotyping. Moreover, we suggest performing intron analysis for the *A105* allele in individuals from Southwestern Korea and Japan, both of which are predominant regions of the *cis-AB* allele.

To the best of our knowledge, we have revealed the first complete genome sequence (except intron 1) of the *cis-ABO1* allele and shown that it arose from the *A105* allele rather than the *A102* allele. Our results are of significance in clarifying the phylogenetic and epidemiologic characteristics of the *cis-ABO1* allele.

Authors' Disclosures of Potential Conflicts of Interest

No potential conflicts of interest relevant to this article were reported.

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